

Amendments to the Claims:

Please amend the claims as shown below. This listing of claims will replace all prior versions and listings of claims in the application.

1. (original) A composition comprising an orthogonal glutamyl-tRNA (glutamyl O-tRNA), wherein the glutamyl O-tRNA comprises at least about a 50% suppression efficiency in the presence of a cognate synthetase in response to a selector codon as compared to the glutamyl O-tRNA corresponding to a polynucleotide sequence as set forth in SEQ ID NO.: 67 (AE(GC) tRNA).
2. (original) The composition of claim 1, wherein the glutamyl O-tRNA comprises a G:C base pair at position 10:28.
3. (original) The composition of claim 1, wherein the selector codon is an amber codon.
4. (original) The composition of claim 1, wherein the glutamyl O-tRNA comprises or is encoded by a polynucleotide sequence as set forth in SEQ ID NO.: 67 (AE(GC) tRNA), or a complementary polynucleotide sequence thereof.
5. (original) The composition of claim 1, further comprising an orthogonal glutamyl aminoacyl-tRNA synthetase (glutamyl O-RS), wherein the glutamyl O-RS preferentially aminoacylates the glutamyl O-tRNA with a selected amino acid in response to the selector codon.
6. (original) The composition of claim 5, wherein the suppression efficiency of the glutamyl O-RS and the glutamyl O-tRNA together is 10 fold greater than the suppression efficiency of the glutamyl O-tRNA in the absence of the glutamyl O-RS.
7. (original) The composition of claim 5, wherein the glutamyl O-RS, or a portion thereof, is encoded by a polynucleotide sequence comprising in any one of SEQ ID NO.: 68 (*Af*), 72 (*Mm*), 74 (*Mt*) or 76 (*Ph*), or a complementary polynucleotide sequence thereof.
8. (original) The composition of claim 5, wherein the glutamyl O-RS comprises an amino acid sequence comprising any one of SEQ ID NO.: 69 (*Af*), 73 (*Mm*), 75 (*Mt*), or 77 (*Ph*), or a conservative variation thereof.

9. (original) The composition of claim 5, wherein the glutamyl O-RS is derived from an organism selected from the group consisting of: an *Archaeoglobus fulgidus* (Af), a *Methanosarcina mazei* (Mm), a *Methanobacterium thermoautotrophicum* (Mt), and a *Pyrococcus horikoshii* (Ph).
10. (original) The composition of claim 1, wherein the glutamyl O-tRNA is derived from one or more archaeal tRNAs.
11. (original) The composition of claim 10, wherein the one or more archaeal tRNAs comprise archaeal glutamyl-tRNA, or derivative thereof.
12. (original) The composition of claim 1, comprising a cell.
13. (original) The composition of claim 12, wherein the cell is an *E. coli* cell.
14. (original) The composition of claim 1, comprising a translation system.
15. (original) A cell comprising a translation system, wherein the translation system comprises:
 - an orthogonal glutamyl-tRNA (glutamyl O-tRNA), wherein the glutamyl O-tRNA comprises at least about a 50% suppression efficiency in the presence of a cognate synthetase in response to a first selector codon as compared to the glutamyl O-tRNA comprising or encoded by a polynucleotide sequence as set forth in SEQ ID NO.: 67 (AE(GC) tRNA);
 - an orthogonal aminoacyl-glutamyl-tRNA synthetase (glutamyl O-RS); and,
 - a first selected amino acid;
 - wherein the glutamyl O-tRNA recognizes the first selector codon, and the glutamyl O-RS preferentially aminoacylates the glutamyl O-tRNA with the first selected amino acid.
16. (original) The cell of claim 15, wherein the glutamyl O-tRNA comprises a G:C base pair at position 10:28.
17. (original) The cell of claim 15, wherein the glutamyl O-tRNA comprises or is encoded by a polynucleotide sequence as set forth in SEQ ID NO.: 67 (AE(GC)), or a complementary polynucleotide sequence thereof, and wherein the glutamyl O-RS comprises an amino acid sequence as set forth in any one of SEQ ID NO.: 69 (Af), 73 (Mm), 75 (Mt), or 77 (Ph), or a conservative variation thereof.

18. (original) The cell of claim 15, wherein the cell further comprises an additional different O-tRNA/O-RS pair and a second selected amino acid, wherein the O-tRNA recognizes a second selector codon and the O-RS preferentially aminoacylates the O-tRNA with the second selected amino acid.

19. (original) The cell of claim 15, wherein the glutamyl O-tRNA is derived from one or more archaeal tRNAs and the glutamyl O-RS is derived from an organism selected from the group consisting of: an *Archaeoglobus fulgidus* (Af), a *Methanosarcina mazei* (Mm), a *Methanobacterium thermoautotrophicum* (Mt), and a *Pyrococcus horikoshii* (Ph).

20. (original) The cell of claim 15, wherein the cell is a non-eukaryotic cell.

21. (original) The cell of claim 20, wherein the non-eukaryotic cell is an *E. coli* cell.

22. (original) The cell of claim 15, further comprising a nucleic acid that comprises a polynucleotide that encodes a polypeptide of interest, wherein the polynucleotide comprises a selector codon that is recognized by the glutamyl O-tRNA.

23. (original) An *E. coli* cell, comprising:

an orthogonal glutamyl tRNA (glutamyl O-tRNA), wherein the glutamyl O-tRNA comprises at least about a 50% suppression efficiency in the presence of a cognate synthetase in response to a selector codon as compared to the glutamyl O-tRNA comprising or encoded by a polynucleotide sequence as set forth in SEQ ID NO.: 67 (AE(GC) tRNA);

an orthogonal glutamyl aminoacyl- tRNA synthetase (glutamyl O-RS), wherein the glutamyl O-RS preferentially aminoacylates the glutamyl O-tRNA with a selected amino acid;

the selected amino acid; and,

a nucleic acid that comprises a polynucleotide that encodes a polypeptide of interest, wherein the polynucleotide comprises the selector codon that is recognized by the glutamyl O-tRNA, and wherein the glutamyl O-tRNA is derived from one or more archaeal tRNAs and the glutamyl O-RS is derived from an organism selected from the group consisting of: an *Archaeoglobus fulgidus* (Af), a *Methanosarcina mazei* (Mm), a *Methanobacterium thermoautotrophicum* (Mt), and a *Pyrococcus horikoshii* (Ph).

24-49. (cancelled)